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=> s triplex and (methylammonium or dimethylammonium or trimethylammonium or tetraethylammonium)

L1 0 TRIPLEX AND (METHYLAMMONIUM OR DIMETHYLAMMONIUM OR TRIMETHYLAMMO
NIUM OR TETRAETHYLAMMONIUM)

=> s triplex and (dimethyl sulfoxide or dmso or polyethylene glycol)

L2 9 TRIPLEX AND (DIMETHYL SULFOXIDE OR DMSO OR POLYETHYLENE GLYCOL)

=> duplicate remove l2

DUPLICATE PREFERENCE IS 'MEDLINE, BIOSIS'
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PROCESSING COMPLETED FOR L2
L3 7 DUPLICATE REMOVE L2 (2 DUPLICATES REMOVED)

=> d 1-7 bib ab

L3 ANSWER 1 OF 7 MEDLINE
AN 2000402358 MEDLINE
DN 20374305 PubMed ID: 10919652
TI Antigene and antiproliferative effects of a c-myc-targeting phosphorothioate triple helix-forming oligonucleotide in human leukemia cells.
AU McGuffie E M; Pacheco D; Carbone G M; Catapano C V
CS Department of Experimental Oncology and Hollings Cancer Center, Medical University of South Carolina, Charleston 29425, USA.
NC CA-70735 (NCI)
SO CANCER RESEARCH, (2000 Jul 15) 60 (14) 3790-9.
Journal code: CNF; 2984705R. ISSN: 0008-5472.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200008
ED Entered STN: 20000901
Last Updated on STN: 20000901
Entered Medline: 20000824
AB The c-myc gene is frequently deregulated and overexpressed in human cancers, and strategies designed to inhibit c-myc expression in cancer cells may have considerable therapeutic value. The purpose of the present work was to characterize the antigene and antiproliferative activity of a triple helix-forming oligonucleotide (TFO) targeted to a homopurine-homopyrimidine sequence in the P2 promoter of the c-myc gene. The TFO was synthesized with phosphorothioate (PS) internucleotide linkages to confer resistance to intra- and extracellular nucleases. This property is required of oligonucleotides designed for in vivo testing and therapeutic applications. The PS-TFO was found to form **triplex** DNA with affinity and specificity comparable with that of the corresponding phosphodiester TFO, as shown by gel mobility shift and footprinting assays. Fluorescence microscopy and polyacrylamide gel analysis showed that the fluorescein-labeled PS-TFO accumulated in nuclei of CEM leukemia cells and remained intact for at least 72 h. Incubation of
CEM cells with PS-TFO reduced c-myc RNA and protein levels. A single exposure of leukemia cells to the PS-TFO was sufficient to induce dose-dependent growth inhibitory effects. Growth inhibition correlated with accumulation of cells in S phase and with induction of cell death by

apoptosis. The PS-TFO was also effective in other leukemia and lymphoma cell lines. Control oligonucleotides had minimal effects in all assays. These data indicate that the c-myc-targeted PS-TFO is an effective antigene and antiproliferative agent, with potential for testing in vivo as a novel approach to cancer therapy.

L3 ANSWER 2 OF 7 MEDLINE DUPLICATE 1
AN 1999107634 MEDLINE
DN 99107634 PubMed ID: 9890933
TI Effects of hydration, ion release, and excluded volume on the melting of **triplex** and duplex DNA.
AU Spink C H; Chaires J B
CS Department of Chemistry, State University of New York, Cortland 13045, USA.
NC CA35635 (NCI)
SO BIOCHEMISTRY, (1999 Jan 5) 38 (1) 496-508.
Journal code: A0G; 0370623. ISSN: 0006-2960.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199902
ED Entered STN: 19990301
Last Updated on STN: 19990301
Entered Medline: 19990218
AB The stability of DNA duplex and **triplex** structures not only depends on molecular forces such as base pairing or tripling or electrostatic interactions but also is sensitive to its aqueous environment. This paper presents data on the melting of Escherichia coli and poly(dA).poly(dT) duplex DNA and on the poly(dT).poly(dA). poly(dT) **triplex** in a variety of media to assess the contributions from the osmotic status and salt content of the media. The effects of volume exclusion on the stability of the DNA structures are also studied. From thermal transition measurements in the presence of low-molecular weight osmotic stressors, the number of water molecules released upon melting is found to be four waters per base pair for duplex melting and one water for the conversion of **triplex** to single-strand and duplex. The effects of Na+ counterion binding are also determined in ethylene glycol solutions so that the variation of counterion binding with water activity is evaluated. The data show that there is a modest decrease in the extent of counterion binding for both duplex and **triplex** as water activity decreases. Finally, using larger **polyethylene glycol** cosolutes, the effects on melting of volume exclusion by the solutes are assessed, and the results correlated with simple geometric models for the excluded volume. These results point out that DNA stability is sensitive to important conditions in the environment of the duplex or **triplex**, and thus, conformation and reactivity can be influenced by these solution conditions.

L3 ANSWER 3 OF 7 MEDLINE DUPLICATE 2
AN 1998121880 MEDLINE
DN 98121880 PubMed ID: 9460548
TI Synthesis and reactivity of aryl nitrogen mustard-oligodeoxyribonucleotide conjugates.
AU Reed M W; Lukhtanov E A; Gorn V; Kutyavin I; Gall A; Wald A; Meyer R B
CS Epoch Pharmaceuticals, Inc., Bothell, Washington 98021, USA.

NC 1-AR-6-2230 (NIAMS)
SO BIOCONJUGATE CHEMISTRY, (1998 Jan-Feb) 9 (1) 64-71.
Journal code: A1T; 9010319. ISSN: 1043-1802.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199803
ED Entered STN: 19980407
Last Updated on STN: 19980407
Entered Medline: 19980323
AB A versatile method is described for preparing aryl nitrogen mustard-oligodeoxyribonucleotide (mustard-ODN) conjugates under anhydrous conditions. The chemistry uses **DMSO** soluble triethylammonium or tributylammonium salts of the ODNs. A G/A motif **triplex** forming ODN was chosen for study since it had been shown earlier to bind with high affinity and specificity to a duplex DNA target. A 5'-hexylamine derivative of this ODN was reacted with three different 2,3,5,6-tetrafluorophenyl ester derivatives of aryl nitrogen mustards which were designed to have different alkylation rates. An HPLC assay was used to determine reaction rates of these mustard-ODNs under various conditions. The reactivity of the mustard groups depended on chloride concentration and the presence of nucleophiles. Conjugation of mustards to G/A-containing ODNs decreased their aqueous stability. Hydrolysis and alkylation rates of these agents were consistent with reaction via an aziridinium intermediate. Rates of sequence specific alkylation within a **triplex** were determined by denaturing gel electrophoresis and shown to depend on inherent reactivity of the mustard group. The improved synthesis and chemical characterization of mustard-ODNs should facilitate their use as sequence specific alkylating agents and as probes for nucleic acid structure.

L3 ANSWER 4 OF 7 MEDLINE
AN 97478543 MEDLINE
DN 97478543 PubMed ID: 9336445
TI **Triplex** formation at physiological pH: comparative studies on DNA **triplexes** containing 5-Me-dC tethered at N4 with spermine and tetraethyleneoxyamine.
AU Rajeev K G; Jadhav V R; Ganesh K N
CS Division of Organic Chemistry, National Chemical Laboratory, Pune 411008, India.
SO NUCLEIC ACIDS RESEARCH, (1997 Nov 1) 25 (21) 4187-93.
Journal code: O8L; 0411011. ISSN: 0305-1048.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199801
ED Entered STN: 19980129
Last Updated on STN: 19980129
Entered Medline: 19980109
AB Oligodeoxynucleotides with spermine conjugation at C4 of 5-Me-dC (sp -ODN) exhibit triple helix formation with complementary Watson-Crick duplexes, and were optimally stable at physiological pH 7.3 and low salt concentration. This was attributed to a favored reassociation of the polycationic third strand with the anionic DNA duplex. To gain further insights into the factors that contribute to the enhancement of

triplex stability and for engineering improved **triplex** systems, the spermine appendage at C4 of 5-Me-dC was replaced with 1,11-diamino-3,6,9-trioxaundecane to create teg -ODNs. From the triple helix forming abilities of these modified ODNs studied by hysteresis behaviour and the effect of salts on **triplex** stability, it is demonstrated here that teg- ODNs stabilise **triplexes** through hydrophobic desolvation while sp -ODNs stabilise **triplexes** by charge effects. The results imply that factors in addition to base stacking effects and interstrand hydrogen bonds are significantly involved in modulation of **triplex** stability by base modified oligonucleotides.

L3 ANSWER 5 OF 7 MEDLINE
AN 97169303 MEDLINE
DN 97169303 PubMed ID: 9016642
TI Radioprobing of DNA: distribution of DNA breaks produced by decay of 125I incorporated into a **triplex**-forming oligonucleotide correlates with geometry of the **triplex**.
AU Panyutin I G; Neumann R D
CS Department of Nuclear Medicine, Warren G.Magnuson Clinical Center, National Institutes of Health, Bethesda , MD 20892, USA.
SO NUCLEIC ACIDS RESEARCH, (1997 Feb 15) 25 (4) 883-7.
Journal code: O8L; 0411011. ISSN: 0305-1048.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
OS PDB-134D
EM 199703
ED Entered STN: 19970327
Last Updated on STN: 19970327
Entered Medline: 19970317
AB The distribution of breaks produced in both strands of a DNA duplex by the decay of 125I carried by a **triplex**-forming DNA oligonucleotide was studied at single nucleotide resolution. The 125I atom was located in the C5 position of a single cytosine residue of an oligonucleotide designed to form a triple helix with the target sequence duplex. The majority of the breaks (90%) are located within 10 bp around the decay site. The addition of the free radical scavenger **DMSO** produces an insignificant effect on the yield and distribution of the breaks. These results suggest that the majority of these breaks are produced by the direct action of radiation and are not mediated by diffusible free radicals. The frequency of breaks in the purine strand was two times higher that in the pyrimidine strand. This asymmetry in the yield of breaks correlates with the geometry of this type of **triplex**; the C5 of the cytosine in the third strand is closer to the sugar-phosphate backbone of the purine strand. Moreover, study of molecular models shows that the yield of breaks at individual bases correlates with distance from the 125I decay site. We suggest the possible use of 125I decay as a probe for the structure of nucleic acids and nucleoprotein complexes.

L3 ANSWER 6 OF 7 BIOSIS COPYRIGHT 2001 BIOSIS
AN 1997:150618 BIOSIS
DN PREV199799449821
TI Radioprobing of DNA: Distribution of DNA breaks produced by decay of 125I incorporated into a **triplex**-forming oligonucleotide correlates

with geometry of the **triplex**.
AU Panyutin, Igor G. (1); Neumann, Ronald D.
CS (1) Dep. Nuclear Med., Warren G. Magnuson Clin. Cent., Natl. Inst. Health,
Bethesda, MD 20892 USA
SO Nucleic Acids Research, (1997) Vol. 25, No. 4, pp. 882-887.
ISSN: 0305-1048.
DT Article
LA English
AB The distribution of breaks produced in both strands of a DNA duplex by the
decay of 125I carried by a **triplex**-forming DNA oligonuclectide
was studied at single nucleotide resolution. The 125I atom was located in the C5 position of a single cytosine residue of an oligonucleotide designed to form a triple helix with the target sequence duplex. The majority of the breaks (90%) are located within 10 bp around the decay site. The addition of the free radical scavenger **DMSO** produces
an insignificant effect on the yield and distribution of the breaks. These
results suggest that the majority of these breaks are produced by the direct action of radiation and are not mediated by diffusible free radicals. The frequency of breaks in the purine strand was two times higher that in the pyrimidine strand. This asymmetry in the yield of breaks correlates with the geometry of this type of **triplex**; the C5 of the cytosine in the third strand is closer to the sugar-phosphate backbone of the purine strand. Moreover, study of molecular models shows that the yield of breaks at individual bases correlates with distance from
the 125I decay site. We suggest the possible use of 125I decay as a probe for the structure of nucleic acids and nucleoprotein complexes.

L3 ANSWER 7 OF 7 MEDLINE
AN 97473519 MEDLINE
DN 97473519 PubMed ID: 9332373
TI Oligodeoxyribonucleotide length and sequence effects on intramolecular and
intermolecular G-quartet formation.
AU Cheng A J; Van Dyke M W
CS Department of Tumor Biology, University of Texas, M.D. Anderson Anderson Cancer Center, Houston 77030, USA.
NC T32 CA60440 (NCI)
SO GENE, (1997 Sep 15) 197 (1-2) 253-60.
Journal code: FOP; 7706761. ISSN: 0378-1119.
CY Netherlands
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199711
ED Entered STN: 19971224
Last Updated on STN: 19971224
Entered Medline: 19971119
AB The potential of guanine-rich oligodeoxyribonucleotides (oligos) as nucleic acid drugs is increasingly being investigated, for example, as aptamers against heparin-binding proteins and as purine-motif **triplex**-forming oligos. However, G-rich oligos can be very polymorphic under physiological conditions, often with the resulting structures possessing vastly different functional capabilities. To better understand the intrinsic oligo parameters that affect their structure, we used nondenaturing gel electrophoresis to investigate a series of G-rich oligos derived from the sequence 5'-TGGGTGGGGTGGGGTGGGT for their

abilities to self-associate through G-quartet formation. From these studies the following observations could be made: (1) oligos containing four clusters of three or more contiguous Gs readily associated intramolecularly but did not associate intermolecularly; (2) intermolecular dimerization was the preferred mode of interaction when one of the oligos contained only two G clusters; and (3) T-rich extensions promoted multimerization of oligos into still higher-order species.

=> s triplex and (phosphate or sulfate or cyanate or isocyanate or isothiocyanate)

L4 209 TRIPLEX AND (PHOSPHATE OR SULFATE OR CYANATE OR ISOCYANATE OR ISOTHIOCYANATE)

=> s l4 and py<1997

L5 146 L4 AND PY<1997

=> duplicate remove l5

DUPLICATE PREFERENCE IS 'MEDLINE, BIOSIS'
KEEP DUPLICATES FROM MORE THAN ONE FILE? Y/(N):n

PROCESSING COMPLETED FOR L5
L6 96 DUPLICATE REMOVE L5 (50 DUPLICATES REMOVED)

=> d bib ab 1-10

L6 ANSWER 1 OF 96 MEDLINE DUPLICATE 1
AN 96278765 MEDLINE
DN 96278765 PubMed ID: 8662935
TI Formation of a combined H-DNA/open TATA box structure in the promoter sequence of the human Na,K-ATPase alpha2 gene.
AU Potaman V N; Ussery D W; Sinden R R
CS Institute of Biosciences and Technology, Texas A&M University, Houston, Texas 77030-3303, USA.
SO JOURNAL OF BIOLOGICAL CHEMISTRY, **(1996 Jun 7)** 271 (23) 13441-7.
Journal code: HIV; 2985121R. ISSN: 0021-9258.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199608
ED Entered STN: 19960911
Last Updated on STN: 19960911
Entered Medline: 19960826
AB Structural variation of DNA within the promoter of the human Na, K-ATPase alpha2 gene, which contains a 35-base pair (bp) homopyrimidine.homopurine (Py.Pu) tract adjacent to a TATA box has been studied. The Py.Pu tract contains a 26-bp quasi-mirror repeat sequence with a potential for intramolecular **triplex** formation. As analyzed by two-dimensional agarose gel electrophoresis, a plasmid containing 151 bp of the promoter sequence including the 35-bp Py.Pu tract undergoes structural transitions under moderately acidic pH. Chemical probing with chloroacetaldehyde, dimethyl **sulfate**, and potassium permanganate is consistent with the formation of **triplex** DNA within the Py.Pu tract at native superhelical density as isolated from Escherichia coli. Chemical probing

was used to determine a supercoil dependence for the formation of this combined unwound structure. At the superhelical density sufficient to locally unwind DNA, an H-y3 isomer of intermolecular **triplex** likely forms. However, at higher superhelical tension an H-y5 structure forms in the Py.Pu tract, and with increasing supercoiling the local DNA unwinding extends into the abutting TATA box. The H-y5/open TATA box combination structure might be favorable at higher superhelical densities since it relaxes more supercoils. The possible involvement of the H-y5/open TATA box structure in transcription is discussed.

L6 ANSWER 2 OF 96 MEDLINE DUPLICATE 2
AN 97027461 MEDLINE
DN 97027461 PubMed ID: 8873600
TI Triple helical structures involving inosine: there is a penalty for promiscuity.
AU Mills M; Volker J; Klump H H
CS Department of Biochemistry, University of Cape Town, Republic of South Africa.
SO BIOCHEMISTRY, **(1996 Oct 15)** 35 (41) 13338-44.
Journal code: A0G; 0370623. ISSN: 0006-2960.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199611
ED Entered STN: 19961219
Last Updated on STN: 19961219
Entered Medline: 19961127
AB Inosine has the ability to act as a "wild-card" binding nonspecifically to
both A.T and G.C base pairs. This has obvious implications for the design of oligonucleotide site-directed probes. In this paper we present a series
of oligonucleotides with a 5'pur9-pyr9-pyr9 motif which are designed to fold up sequentially into intramolecular triple helices. One or more inosines are incorporated into the Hoogsteen strands in place of T's and/or C's. Once folded into the **triplex**, the inosine-containing third strand is incorporated in parallel orientation to the purine strand of the duplex. The influence of inosine on the **triplex**-duplex equilibrium, characterized by the melting temperature (Tm) and on the phase boundaries, as a function of pH and/or ionic strength, has been assessed by means of UV and CD spectroscopy. There are two distinguishable
influences of third-strand inosines which affect binding, namely, backbone
distortion due to bulkiness (I for T and I for C+) and/or loss of intramolecular ion pairs between protonated cytosines and the backbone **phosphates** (I for C+). A single thymine replacement drops the Tm by 25.0 (+/- 2.1) degrees C, and replacing a single protonated cytosine drops the Tm by 32.1 (+/- 1.0) degrees C at pH 6.0. On introducing two inosines in place of thymines, the Tm at pH 6.0 of the triple helix to hairpin transition is lowered by 35.5 (+/- 1.4) degrees C; on introducing two inosines in place of cytosines, the Tm drops by 44.5 (+/- 1.0) degree C, and on replacing a cytosine and a neighboring thymine with inosines, the Tm of the same transition is lowered by 29.2 (+/- 1.6) degrees C. Replacing more than two thymines or cytosines, respectively, eliminates the binding of the Hoogsteen strand at room temperature altogether. Under no circumstances does inosine replacement stabilize the **triplex** helix: it is a poor substitute and its role as a wild-card is limited.

L6 ANSWER 3 OF 96 MEDLINE DUPLICATE 3
AN 97027460 MEDLINE
DN 97027460 PubMed ID: 8873599
TI Alternate-strand **triplex** formation: modulation of binding to matched and mismatched duplexes by sequence choice in the Pu-Pu-Py block.
AU Balatskaya S V; Belotserkovskii B P; Johnston B H
CS Cell and Molecular Biology Laboratory, SRI International, Mento Park, California 94025, USA.
NC GM48863 (NIGMS)
SO BIOCHEMISTRY, **(1996 Oct 15)** 35 (41) 13328-37.
Journal code: A0G; 0370623. ISSN: 0006-2960.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199611
ED Entered STN: 19961219
Last Updated on STN: 19961219
Entered Medline: 19961127
AB In double-stranded DNA, tandem blocks of purines (Pu) and pyrimidines (Py) can form **triplexes** by pairing with oligonucleotides which also consist of blocks of purines and pyrimidines, using both Py.Pu.Py (Y-type) and Pu.Pu.Py (R-type) pairing motifs in a scheme called "alternate-strand recognition," or ASR [Jayasena, S. D., & Johnston, B. H. (1992) Biochemistry 31, 320-327; Beal P. A., & Dervan, P. B. (1992) J. Am. Chem. Soc. 114, 1470-1478]. We investigated the relative contributions of the Py.Pu.Py and Pu.Pu.Py blocks in the 16-bp duplex sequence 5'-AAGGAGAATTCCCTCT-3' paired with the third-strand oligonucleotides 5'-TTCCTCTTXXGGGZGZ-3' (XZ-16), where X and Z are either T or A and C is 5-methylcytosine, using chemical footprinting and get electrophoretic mobility shift measurements. We found that the left-hand, pyrimidine half (Y-block) of the third strand (TTCCTCTT, Y-8) forms a Py.Pu.Py **triplex** as detected by both dimethyl **sulfate** (DMS) probing and a gel-shift assay; in contrast, the **triplex** formed by the right-hand half alone (R-block) with X = T (TTGGGTGT, R-8) is not detectable under the conditions tested. However, when tethered to the Y-block (i.e., as XZ-16), the R-block contributes greatly increased specificity of target recognition and confers protection from DMS onto the duplex even under conditions unfavorable for Pu-Pu-Py **triplexes** (lack of divalent cations). In general, the 16-mer (XZ-16) can bind with apparent strength either greater or lesser than Y-8, depending on whether X and Z are A or T. The order of apparent binding strength, as measured by the target duplex concentration necessary to cause retardation of the third strand during gel electrophoresis, is TT-16 approximately AT-16 > Y-8 > AA-16 > TA-16. Chemical probing experiments showed that both halves of the **triplex** form even for AA-16, which binds with less apparent binding strength than the pyrimidine block alone (Y-8). The presence of the right half of the 16-mers, although detracting from affinity in cases of AA-16 and TA-16, provides strong specificity for the correct target compared to a target incapable of forming the Pu.Pu.Py part of the **triplex**. We discuss possible explanations for these observations in terms of alternate oligonucleotide conformations and suggest practical applications of affinity modulation by A-to-T replacements.

L6 ANSWER 4 OF 96 MEDLINE
AN 96420466 MEDLINE
DN 96420466 PubMed ID: 8823165
TI Sequence-specific alkylation and cleavage of DNA mediated by purine motif triple helix formation.
AU Grant K B; Dervan P B
CS Beckman Institute, California Institute of Technology, Pasadena 91125, USA.
NC GM-16965-02 (NIGMS)
GM-81747 (NIGMS)
SO BIOCHEMISTRY, **(1996 Sep 24)** 35 (38) 12313-9.
Journal code: A0G; 0370623. ISSN: 0006-2960.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199611
ED Entered STN: 19961219
Last Updated on STN: 19961219
Entered Medline: 19961105
AB An N-bromoacetyl electrophile attached to the 5'-**phosphate** group of a purine-rich oligonucleotide affords sequence-specific alkylation of duplex DNA (at 37 degrees C, pH 7.4) through the formation of a specific purine.purine.pyrimidine triple-helical complex. In a 645 bp restriction fragment containing three consecutive guanine bases adjacent to the 3'-end of an oligonucleotide binding site, the yield of single-strand cleavage after piperidine treatment is 80% at the guanine base directly adjacent to the binding site and 88% overall. In an 837 bp restriction fragment containing two adjacent inverted repeats of the third strand binding site and a single 3'-guanine base, yields of single-strand cleavage are 97% on each strand at the 3'-guanine base. Double-strand cleavage was obtained in 61% yield at a single site in a 6.6 kbp plasmid containing the 837 bp fragment. Extension of triple helix mediated DNA alkylation from the pyrimidine to purine motif formally extends the number of sites in duplex DNA that can be cleaved in a sequence-specific and nucleotide-specific manner in good yields.

L6 ANSWER 5 OF 96 BIOSIS COPYRIGHT 2001 BIOSIS
AN 1996:503347 BIOSIS
DN PREV199699225703
TI Synthesis of C-branched spermine tethered oligo-DNA and the thermal stability of the duplexes and **triplexes**.
AU Sund, Christian; Puri, Nitin; Chattopadhyaya, Jyoti (1)
CS (1) Dep. Bioorganic Chemistry, Box 581, Biomedical Cent., Univ. Uppsala, S-751 23 Uppsala Sweden
SO Tetrahedron, (1996) Vol. 52, No. 37, pp. 12275-12290.
ISSN: 0040-4020.
DT Article
LA English
AB The first synthesis of the new C-branched spermine derivative 17, as well as its ability to stabilise DNA duplexes and **triplexes**, are reported. The C-branched spermine block 17 was converted into the corresponding O-(2-cyanoethyl)-(N,N-diisopropyl)phosphoranidite block 18 for incorporation at the 5'-end of DNA. It was also coupled to the 2' of ara-U through a **phosphate** bridge, leading to the partially protected 3'-hydroxy block 23, which was either converted to the

O-(2-cyanoethyl)-(N,N-diisopropyl)phosphoramidite 24 or to the 3'-succinate block 25, leading to the synthesis of three model DNA 14-mers: 27 with tethered spermine at the 5'-end, 28 with tethered spermine at the middle of the DNA strand, and 29 with spermine at the 2'-end, using standard automated solid-phase chemistry and deprotection procedures. The T-m measurements showed that, at low salt with Mg-2+ within the pH range of 5.5 - 7.6, the 5'-spermine-DNA conjugate 27 gives stabilised DNA **triplexes** with DELTA-hT-m s of apprx +3 degree C and DELTA-cT-m s of +5.5 degree to +8.5 degree C and the 2'-spermine-DNA conjugate 29 gives DELTA-hT-m s of apprx +5 degree to +6.5 degree C and DELTA-cT-m s of +7.5 degree to +9 degree C over the underivatised DNA counterpart 30. In contrast, the spermine block conjugated to the middle of the DNA as in 28 gave no **triplex** formation. Without Mg-2+, these short T-rich oligonucleotides (27, 29 & 30) gave **triplex** formation only above 0.4M NaCl. At 1.4M, the DELTA-hT-m s for 27 and 29 over 30 were +9.5 degree C while the DELTA-cT-m s were +6 degree to +7 degree C. Oligonucleotide conjugates 27 & 29 gave only weak duplex stabilisations with DELTA-hT-m s of apprx +2 degree and apprx +1 degree C, respectively, over 30 at low salt with Mg-2+ within the pH range 5.5 - 7.6.

L6 ANSWER 6 OF 96 MEDLINE DUPLICATE 4
AN 96291255 MEDLINE
DN 96291255 PubMed ID: 8703918
TI Distamycin A complexation with a nucleic acid triple helix.
AU Durand M; Maurizot J C
CS Centre de Biophysique Moleculaire, Universite d'Orleans, France.
SO BIOCHEMISTRY, **(1996 Jul 16)** 35 (28) 9133-9.
Journal code: A0G; 0370623. ISSN: 0006-2960.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199609
ED Entered STN: 19960919
Last Updated on STN: 19960919
Entered Medline: 19960912
AB The interaction of the minor groove binding drug distamycin with the T-A-T triple helix and the A-T double helix was studied using circular dichroism spectroscopy and thermal denaturation. The triple helix was made by the oligonucleotide (dA)12-x-(dT)12-x-(dT)12, where x is a hexaethylene glycol chain bridged between the 3'-**phosphate** of one strand and the 5'-**phosphate** of the following strand. This oligonucleotide is able to fold back on itself to form a very stable **triplex**. Changing the conditions allows the same oligonucleotide to be in a duplex form with a dangling arm. Circular dichroism spectroscopy demonstrates that the distamycin A molecule can bind to the triple-stranded form of this oligonucleotide. Spectral analysis shows that the bound distamycin exhibits a conformation and an environment slightly different from those which are observed when the drug is bound to the corresponding double-stranded structure. Furthermore, a second type of complex which is observed in the double-strand binding (two stacked distamycins in the minor groove) is not observed with the triple-stranded host. When distamycin is added to the **triplex** made of unbridged chains (dA)12 + 2(dT)12, the **triplex** dissociates to give a double-stranded structure. Thermal denaturation experiments demonstrate

that distamycin binding destabilizes the **triplex** whereas it stabilizes the duplex. These results are compared with those obtained by the same experimental approaches on other minor groove binding drugs.

L6 ANSWER 7 OF 96 MEDLINE DUPLICATE 5
AN 97048022 MEDLINE
DN 97048022 PubMed ID: 8892863
TI Cytomegalovirus "missing" capsid protein identified as heat-aggregable product of human cytomegalovirus UL46.
AU Gibson W; Baxter M K; Clopper K S
CS Virology Laboratories, Department of Pharmacology and Molecular Sciences, The Johns Hopkins University School of Medicine, Baltimore, Maryland 21205, USA.. Wade_Gibson@qmail.bs.jhu.edu
NC AI13718 (NIAID)
AI32957 (NIAID)
T32 GM07445 (NIGMS)
SO JOURNAL OF VIROLOGY, **(1996 Nov)** 70 (11) 7454-61.
Journal code: KCV; 0113724. ISSN: 0022-538X.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199612
ED Entered STN: 19970128
Last Updated on STN: 19970128
Entered Medline: 19961230
AB Capsids of human and simian strains of cytomegalovirus (HCMV and SCMV, respectively) have identified counterparts for all but one of the protein components of herpes simplex virus (HSV) capsids. The open reading frames (ORFs) for the CMV and HSV counterpart proteins are positionally homologous in the two genomes. The HSV capsid protein without a recognized counterpart in CMV is VP19c, a 50-kDa element of the intercapsomeric " **triplex**." VP19c is encoded by HSV ORF UL38, whose positional homolog in the HCMV genome is UL46. The predicted protein product of HCMV UL4A6, however, has essentially no amino acid sequence similarity to HSV VP19c, is only two-thirds as long, and was not recognized as a component of CMV capsids. To identify and learn more about the protein encoded by HCMV UL46, we have expressed it in insect cells from a recombinant baculovirus and tested for its presence in CMV-infected human cells and virus particles with two UL4A6-specific antipeptide antisera. Results presented here show that this HCMV protein (i) has a size of approximately 30 kDa as expressed in both recombinant baculovirus-infected insect cells and HCMV-infected human cells; (ii) has a homolog in SCMV; (iii) is a capsid component and is present in a 1:2 molar ratio with the minor capsid protein (mCP), encoded by UL85; and (iv) interacts with the mCP, which is also shown to interact with itself as demonstrated by the GAL4 two-hybrid system; and (v) aggregates when heated and does not enter the resolving gel during sodium dodecyl **sulfate**-polyacrylamide gel electrophoresis (SDS-PAGE), a characteristic that accounts for it eluding detection until now. We call this protein the mCP-binding protein, and on the basis of the characteristics that it shares with HSV VP19c, we conclude that the HCMV mCP-binding protein is the functional as well as genetic homolog of HSV VP19c.

L6 ANSWER 8 OF 96 MEDLINE
AN 97105896 MEDLINE
DN 97105896 PubMed ID: 8948644

TI Interstrand cross-linking reaction in **triplexes** containing a monofunctional transplatin-adduct.
AU Colombier C; Lippert B; Leng M
CS Centre de Biophysique Moleculaire, CNRS, Orleans, France.
SO NUCLEIC ACIDS RESEARCH, **(1996 Nov 15)** 24 (22) 4519-24.
Journal code: O8L; 0411011. ISSN: 0305-1048.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199701
ED Entered STN: 19970219
Last Updated on STN: 19970219
Entered Medline: 19970117
AB Our aim was to determine whether a single transplatin monofunctional adduct, either trans-[Pt(NH3)2(dC)Cl]+ or trans-[Pt(NH3)2(dG)Cl]+ within a
homopyrimidine oligonucleotide, could further react and form an interstrand cross-link once the platinated oligonucleotide was bound to the complementary duplex. The single monofunctional adduct was located at either the 5' end or in the middle of the platinated oligonucleotide. In all the **triplexes**, specific interstrand cross-links were formed between the platinated Hoogsteen strand and the complementary purine-rich strand. No interstrand cross-links were detected between the platinated oligonucleotides and non-complementary DNA. The yield and the rate of the cross-linking reaction depend upon the nature and location of the monofunctional adducts. Half-lives of the monofunctional adducts within the **triplexes** were in the range 2-6 h. The potential use of the platinated oligonucleotides to modulate gene expression is discussed.

L6 ANSWER 9 OF 96 MEDLINE
AN 96292267 MEDLINE
DN 96292267 PubMed ID: 8692703
TI **Triplex** formation by oligonucleotides containing novel deoxycytidine derivatives.
CM Erratum in: Nucleic Acids Res 1997 Sep 15;25(18):following 3750
AU Huang C Y; Bi G; Miller P S
CS Department of Biochemistry, School of Hygiene and Public Health, The Johns
Hopkins University, Baltimore, MD 21205, USA.
NC GM27512 (NIGMS)
GM45012 (NIGMS)
RR06262 (NCRR)
SO NUCLEIC ACIDS RESEARCH, **(1996 Jul 1)** 24 (13) 2606-13.
Journal code: O8L; 0411011. ISSN: 0305-1048.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199608
ED Entered STN: 19960911
Last Updated on STN: 19990129
Entered Medline: 19960827
AB Homopurine sequences of duplex DNA are binding sites for **triplex**-forming oligodeoxyribopyrimidines. The interactions of synthetic duplex DNA targets with an oligodeoxyribopyrimidine containing N4-(6-amino-2-pyridinyl)deoxycytidine (1), a nucleoside designed to interact with a single C-G base pair interruption of the purine target tract, was studied by UV melting, circular dichroism spectroscopy and dimethylsulfate alkylation experiments. Nucleoside 1 supports stable

triplex formation at pH 7.0 with formation of a 1-Y-Z triad, where Y-Z is a base pair in the homopurine tract of the target. Selective interaction was observed when Y-Z was C-G, although A-T and, to a lesser extent, T-A and G-C base pairs were also recognized. The circular dichroism spectra of the **triplex** having a 1-C-G triad were similar to those of a **triplex** having a C(+)-G-C triad, suggesting that the overall structures of the two **triplexes** are quite similar. Removal of the 6-amino group from 1 essentially eliminated **triplex** formation. Reaction of a **triplex** having the 1-C-G triad with dimethylsulfate resulted in a 50% reduction of methylation of the G residue of this triad. In contrast, the G of a similar **triplex** containing a U-C-G triad was not protected from methylation by dimethylsulfate. These results are consistent with a binding mode in which the 6-amino-2-pyridinyl group of 1 spans the major groove of the target duplex at the 1-C-G binding site and forms a hydrogen bond with the O6 of G. An additional stabilizing hydrogen bond could form between the N4 of the imino tautomer of 1 and the N4 amino group of C.

L6 ANSWER 10 OF 96 MEDLINE DUPLICATE 6
AN 96211383 MEDLINE
DN 96211383 PubMed ID: 8649997
TI Binding of DNA oligonucleotides to sequences in the promoter of the human bcl-2 gene.
AU Olivas W M; Maher L J 3rd
CS Eppley Institute for Research in Cancer and Allied Diseases, University of Nebraska Medical Center, Omaha, USA.
NC GM 47814 (NIGMS)
SO NUCLEIC ACIDS RESEARCH, **(1996 May 1)** 24 (9) 1758-64.
Journal code: O8L; 0411011. ISSN: 0305-1048.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199607
ED Entered STN: 19960805
Last Updated on STN: 19960805
Entered Medline: 19960725
AB Duplex DNA recognition by oligonucleotide-directed triple helix formation is being explored as a highly specific approach to artificial gene repression. We have identified two potential **triplex** target sequences in the promoter of the human bcl-2 gene, whose product inhibits apoptosis. Oligonucleotides designed to bind these target sequences were tested for their binding affinities and specificities under pseudo-physiological conditions. Electrophoretic mobility shift and dimethyl **sulfate** footprinting assays demonstrated that an oligonucleotide designed for simultaneous recognition of homopurine domains on alternate duplex DNA strands had the highest affinity of any oligonucleotide tested. Modifications to render this oligonucleotide nuclease-resistant did not reduce its binding affinity or specificity. In additional studies under various pH conditions, pyrimidine motif complexes at these target sequences were found to be stable at pH 8.0, despite the presumed requirement for protonation of oligonucleotide cytidines. In contrast, purine motif complexes, typically considered to be pH independent, were highly destabilized at decreasing pH values. These results indicate that a natural sequence in the human bcl-2 promoter can form a stable **triplex** with a synthetic oligonucleotide under pseudo-physiological conditions, and suggest that triple helix formation

might provide an approach to the artificial repression of bcl-2 transcription.

=> d his

(FILE 'HOME' ENTERED AT 17:48:25 ON 09 AUG 2001)

FILE 'MEDLINE, BIOSIS' ENTERED AT 17:48:46 ON 09 AUG 2001
L1 0 S TRIPLEX AND (METHYLAMMONIUM OR DIMETHYLAMMONIUM OR TRIMETHYLA
L2 9 S TRIPLEX AND (DIMETHYL SULFOXIDE OR DMSO OR POLYETHYLENE GLYCO
L3 7 DUPLICATE REMOVE L2 (2 DUPLICATES REMOVED)
L4 209 S TRIPLEX AND (PHOSPHATE OR SULFATE OR CYANATE OR ISOCYANATE OR
L5 146 S L4 AND PY>1997
L6 96 DUPLICATE REMOVE L5 (50 DUPLICATES REMOVED)

=> s triple helix and (methylammonium or dimethylammonium or trimethylammonium or tetraethylammonium)

L7 3 TRIPLE HELIX AND (METHYLAMMONIUM OR DIMETHYLAMMONIUM OR TRIMETHY
LAMMONIUM OR TETRAETHYLAMMONIUM)

=> d 1-3 bib ab

L7 ANSWER 1 OF 3 MEDLINE
AN 96125132 MEDLINE
DN 96125132 PubMed ID: 8537413
TI Novel polyaminolipids enhance the cellular uptake of oligonucleotides.
AU Guy-Caffey J K; Bodepudi V; Bishop J S; Jayaraman K; Chaudhary N
CS Aronex Pharmaceuticals, Inc., The Woodlands, Texas 77381, USA.
SO JOURNAL OF BIOLOGICAL CHEMISTRY, (1995 Dec 29) 270 (52) 31391-6.
Journal code: HIV; 2985121R. ISSN: 0021-9258.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199602
ED Entered STN: 19960221
Last Updated on STN: 19960221
Entered Medline: 19960208
AB Two new polyaminolipids have been synthesized for the purpose of improving
cellular uptake of oligonucleotides. The amphipathic compounds are conjugates of spermidine or spermine linked through a carbamate bond to cholesterol. The polyaminolipids are relatively nontoxic to mammalian cells. In tissue culture assays, using fluorescent-tagged or radiolabeled **triple helix**-forming oligonucleotides, spermine-cholesterol and spermidine-cholesterol significantly enhance cellular uptake of the oligomers in the presence of serum. Spermine-cholesterol is comparable with DOTMA/DOPE (a 1:1 (w/w) formulation of the cationic lipid N-[1-(2,3-dioleyloxy)-propyl]-N,N,N-**trimethylammonium** chloride (DOTMA) and the neutral lipid dioleylphosphatidylethanolamine (DOPE)) in increasing cellular uptake of oligonucleotides, while spermidine-cholesterol is more efficient. The

internalized oligonucleotides are routed to the nucleus as early as 20 min after treatment, suggesting that the polyaminolipids increase the permeability of cellular membranes to oligonucleotides. At later times, much of the incoming oligonucleotides are sequestered within punctate cytoplasmic granules, presumably compartments of endosomal origin. Coadministration with polyaminolipids markedly improves the cellular stability of the oligonucleotides; more than 80% of the material can be recovered intact up to 24 h after addition to cells. In the absence of the polyaminolipids, nearly all of the material is degraded within 6 h. These data suggest that the new polyaminolipids may be useful for the delivery of nucleic acid-based therapeutics into cells.

L7 ANSWER 2 OF 3 MEDLINE
AN 76253621 MEDLINE
DN 76253621 PubMed ID: 952887
TI Poly(2-aminoadenylic acid): interaction with poly(uridylic acid).
AU Howard F B; Frazier J; Miles H T
SO BIOCHEMISTRY, (1976 AUG 24) 15 (17) 3783-95.
Journal code: A0G; 0370623. ISSN: 0006-2960.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 197611
ED Entered STN: 19900313
Last Updated on STN: 19900313
Entered Medline: 19761101
AB Poly(2-aminoadenylic acid) forms both double and **triple helices** with poly(uridylic acid) [poly(U)]. The 2-amino group forms a third hydrogen bond, elevating the 2 leads to 1 transition temperature by 33 degrees C. The third strand, however, has about the same stability as poly(A)-2poly(U), as measured by Tm 3 leads to 2. This selective stabilization of the two-stranded helix results in a much greater resolution of the differnt thermal transitions than that observed in analogous polynucleotide systems. In contrast to other A, U systems 3 leads to 1 and 2 leads to 3 transitions are not observed under any conditions, and the **triple helix** always undergoes a 3 leads to 2 transition even at very high ionic strength. A 1:1 mixture of poly(2NH2A) and poly(U) exhibits no transient formation of 1:2 complex, unlike similar mixtures of poly(A) with poly(U) and poly(T). This difference is evidently due to a more rapid displacement reaction: [poly(2NH2A) + poly(2NH2A)-2poly(U) leads to 2 poly(2NH2A)-poly(U)] With poly(2NH2A) than with poly(A). We describe a method for establishing the combining ratios of polynucleotide complexes which used a computer to calculate the angles of intersection of mixing curves as explicit and continuous functions of the wavelength. The wavelength dispersions of the angles of intersection determine optimum wavelengths for establishing stoichiometry and can also provide reliable negative evidence that presumably plausible complexes are not formed. Analogous computer procedures have been developed to determine wavelengths which are selective for the formation of both 1:1 and 1:2 complexes. Infrared spectra of the 1:1 and 1:2 complexes resemble those of other A, U homoribopolynucleotide helices in having two and three strong bands, respectively, in the region of carbonyl stretching vibrations. CD spectra of the two complexes are unusual in having negative first extrema of moderate intensity. We attribute these extrema to intrastrand interactions

of strong, well-resolved transitions at 278 nm (B2u) of the 2-aminoadenine residues. The CD spectra are correlated with those of other polynucleotide helices.

L7 ANSWER 3 OF 3 BIOSIS COPYRIGHT 2001 BIOSIS
AN 1996:76343 BIOSIS
DN PREV199698648478
TI Novel polyaminolipids enhance the cellular uptake of oligonucleotides.
AU Guy-Caffey, Judith K.; Bodepudi, Veeraiah; Bishop, Jeffrey S.; Jayaraman, Krishna; Chaudhary, Nilabh (1)
CS (1) Aronex Pharmaceuticals Inc., 3400 Research Forest Drive, The Woodlands, TX 77381 USA
SO Journal of Biological Chemistry, (1995) Vol. 270, No. 52, pp. 31391-31396.
ISSN: 0021-9258.
DT Article
LA English
AB Two new polyaminolipids have been synthesized for the purpose of improving cellular uptake of oligonucleotides. The amphipathic compounds are conjugates of spermidine or spermine linked through a carbamate bond to cholesterol. The polyaminolipids are relatively nontoxic to mammalian cells. In tissue culture assays, using fluorescent-tagged or radiolabeled **triple helix**-forming oligonucleotides, spermine-cholesterol and spermidine-cholesterol significantly enhance cellular uptake of the oligomers in the presence of serum. Spermine-cholesterol is comparable with DOTMA/DOPE (a 1:1 (w/w) formulation of the cationic lipid N-(1-(2,3-di-oleyloxy)-propyl)-N,N,N-**trimethylammonium** chloride (DOTMA) and the neutral lipid dioleylphosphatidylethanolamine (DOPE)) in increasing cellular uptake of oligonucleotides, while spermidine-cholesterol is more efficient. The internalized oligonucleotides are routed to the nucleus as early as 20 min after treatment, suggesting that the polyaminolipids increase the permeability of cellular membranes to oligonucleotides. At later times, much of the incoming oligonucleotides are sequestered within punctate cytoplasmic granules, presumably compartments of endosomal origin. Coadministration with polyaminolipids markedly improves the cellular stability of the oligonucleotides; more than 80% of the material can be recovered intact up to 24 h after addition to cells. In the absence of the polyaminolipids, nearly all of the material is degraded within 6 h. These data suggest that the new polyaminolipids may be useful for the delivery of nucleic acid-based therapeutics into cells.

=> s triple helix and (phosphate or sulfate or cyanate or isocyanate or isothiocyanate)

L8 190 TRIPLE HELIX AND (PHOSPHATE OR SULFATE OR CYANATE OR ISOCYANATE OR ISOTHIOCYANATE)

=> s l8 and py<1997

L9 143 L8 AND PY<1997

=> s l8 and py<1996

L10 119 L8 AND PY<1996

=> duplicate remove l10

DUPLICATE PREFERENCE IS 'MEDLINE, BIOSIS'
KEEP DUPLICATES FROM MOPE THAN ONE FILE? Y/(N):n

PROCESSING COMPLETED FOR L10
L11 73 DUPLICATE REMOVE L10 (46 DUPLICATES REMOVED)

=> d bib ab 1-10

L11 ANSWER 1 OF 73 BIOSIS COPYRIGHT 2001 BIOSIS
AN 1995:374088 BIOSIS
DN PREV199598388388
TI DNA analogues with nonphosphodiester backbones.
AU Nielsen, Peter E.
CS Cent. Biomol. Recognition, Dep. Med. Biochem. Genetics, Biochemistry Lab. B, Univ. Copenhagen, Panum Inst., Blegdamsvej 3, DK-2200 Copenhagen N Denmark
SO Stroud, R. M. [Editor]. Annual Review of Biophysics and Biomolecular Structure, (1995) Vol. 24, pp. 167-183. Annual Review of Biophysics and Biomolecular Structure.
Publisher: Annual Reviews Inc. P.O. Box 10139, 4139 El Camino Way, Palo Alto, California 94306, USA.
ISSN: 1056-8700. ISBN: 0-8243-1824-2.
DT Book; General Review
LA English

L11 ANSWER 2 OF 73 MEDLINE DUPLICATE 1
AN 95294012 MEDLINE
DN 95294012 PubMed ID: 7775467
TI An unusually stable purine(purine-pyrimidine) short triplex. The third strand stabilizes double-stranded DNA.
AU Svinarchuk F; Paoletti J; Malvy C
CS Laboratoire de Biochimie-Enzymologie, CNRS URA 147, Institute Gustave Roussy, Villejuif, France.
SO JOURNAL OF BIOLOGICAL CHEMISTRY, **(1995 Jun 9)** 270 (23) 14068-71.
Journal code: HIV; 2985121R. ISSN: 0021-9258.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199507
ED Entered STN: 19950720
Last Updated on STN: 19950720
Entered Medline: 19950710
AB Classical models for DNA **triple helix** formation assume the stabilization of these structures through the formation of Hoogsteen hydrogen bonds. This assumes that G-rich duplex DNA is more stable than triplex DNA. We report the results of co-migration assay, dimethyl **sulfate** footprint, and UV spectroscopic melting studies that reveal that at least in some cases of short (13-mer) purine(purine-pyrimidine) triplex the stability of double-stranded DNA is increased by the binding of the third strand. Under conditions which are usually considered as physiological (10 mM MgCl2, 150 mM Na+ or K+) and with a rate of heating/cooling of 1 degrees C/min, there is a good reversibility of the melting profiles which is consistent with a high rate of triplex

formation. Other factors than Hoogsteen hydrogen bonds should therefore be involved in triplex stabilization. We suggest that oligonucleotides with similar properties could be efficient agents for artificial gene regulation.

L11 ANSWER 3 OF 73 MEDLINE DUPLICATE 2
AN 95263411 MEDLINE
DN 95263411 PubMed ID: 7744733
TI Two heparin-binding domains are present on the collagenic tail of asymmetric acetylcholinesterase.
AU Deprez P N; Inestrosa N C
CS Departamento de Biologia Celular y Molecular, Facultad de Ciencias Biologicas, Pontificia Universidad Catolica de Chile, Santiago.
SO JOURNAL OF BIOLOGICAL CHEMISTRY, **(1995 May 12)** 270 (19) 11043-6.
Journal code: HIV; 2985121R. ISSN: 0021-9258.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199506
ED Entered STN: 19950621
Last Updated on STN: 19980206
Entered Medline: 19950615
AB The collagen-tailed form of acetylcholinesterase (AChE) binds to heparin and heparan **sulfate** proteoglycans. We have employed synthetic peptides corresponding to the central collagenic region of the tail of AChE, to identify the heparin-binding domains of the tail of asymmetric AChE. Two putative heparin-binding consensus sequences were localized in the collagenic tail. Peptides containing such sequences (P-(145-159) and P-(249-262)) were able to release asymmetric AChE bound to heparin-agarose. A triple mutation, Asn-Asp-Gly-Gly instead of Arg-His-Gly-Arg, completely abolishes the capacity of the peptide P-(145-159) to elute AChE from the heparin column. Our results suggest that the interaction between the collagen-tailed AChE and proteoglycans is mediated by clusters of basic residues that form two belts around the **triple helix** of the collagenic tail.

L11 ANSWER 4 OF 73 MEDLINE DUPLICATE 3
AN 96091203 MEDLINE
DN 96091203 PubMed ID: 7501477
TI Single strand targeted triplex formation: targeting purine-pyrimidine mixed sequences using abasic linkers.
AU Kandimalla E R; Manning A N; Venkataraman G; Sasisekharan V; Agrawal S
CS Hybridon, Inc., Worcester, MA 01605, USA.
SO NUCLEIC ACIDS RESEARCH, **(1995 Nov 11)** 23 (21) 4510-7.
Journal code: O8L; 0411011. ISSN: 0305-1048.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199601
ED Entered STN: 19960217
Last Updated on STN: 19980206
Entered Medline: 19960117
AB Foldback triplex-forming oligonucleotides (FTFOs) that contain an abasic linker, [2-(4-aminobutyr-1-yl)-1,3-propanediol] (APD linker), in the Hoogsteen domain against pyrimidine bases of a C:G and a T:A base pair were studied for their relative stability and sequence specificity of

triplex formation. In general, the APD linker has less destabilizing effect against a C:G base pair than a T:A base pair. Incorporation of three APD linker moieties resulted in decreased binding to the target, which was comparable to results observed with three imperfectly matched natural base triplets. The APD linker incorporation did not result in the loss of sequence specificity of FTFOs, unlike in the case of normal triplex-forming oligonucleotides (TFOs). The introduction of a positively charged abasic linker, however, resulted in decreased stability of the triplex, because of loss of hydrogen bonding and stacking interactions in the major groove. The results of a molecular modeling study show that APD linker can be readily incorporated without any change in the conformation of the natural sugar-**phosphate** backbone conserving overall **triple helix** geometry. Further, the modeling study suggests a hydrogen bond formation between the amino group of linker and N4 of cytosine mediated by a solvent molecule (water) in the floor of the base triplet in addition to a contribution from the positive charge on the APD linker amino group. Either a direct or water-mediated hydrogen bond between the amino group of the APD linker and the O4 of thymine is unlikely when the linker is placed against a T:A base pair.

L11 ANSWER 5 OF 73 MEDLINE DUPLICATE 4
AN 95210279 MEDLINE
DN 95210279 PubMed ID: 7535100
TI Origins of the large differences in stability of DNA and RNA helices: C-5 methyl and 2'-hydroxyl effects.
AU Wang S; Kool E T
CS Department of Chemistry, University of Rochester, New York 14627 USA.
SO BIOCHEMISTRY, **(1995 Mar 28)** 34 (12) 4125-32.
Journal code: A0G; 0370623. ISSN: 0006-2960.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199505
ED Entered STN: 19950510
Last Updated on STN: 19960129
Entered Medline: 19950502
AB Recent studies have shown that there can be large differences in the stability of double and triple helical nucleic acid complexes, depending on whether RNA or DNA strands are involved. These differences have been attributed to structural differences in the sugar-**phosphate** backbone of these two polymers. However, since there are in fact two structural features which distinguish DNA from RNA (the 2'-hydroxyl and C-5 methyl groups), the stability differences may arise from either or both of these factors. We have separated effects of the 2'-hydroxyl and C-5 methyl groups by synthesizing nucleic acid strands which contain all possible combinations with and without these groups. Studies of the stabilities of double and **triple helices** involving these strands show that in fact the C-5 methyl group of thymine and the 2'-OH group of ribose have equally large effects on stability. The two effects vary with secondary structure and can be reinforcing or even opposing in their influence on stability. Three types of complexes are specifically examined: bimolecular pyrimidine.purine duplexes, termolecular pyrimidine.purine.pyrimidine triplexes, and bimolecular triplexes formed from circular pyrimidine oligonucleotides with purine target strands. It is found in general that the two types of substitutional effects are independent of one another and that C-5 methyl groups are in all cases stabilizing, while 2'-OH groups can be stabilizing

or destabilizing, depending on the type of complex. In addition, studies with partially methylated duplexes lend evidence that the largest contribution to stabilization by the methyl group arises from increased base stacking ability rather than from a favorable hydrophobic methyl-methyl contact.(ABSTRACT TRUNCATED AT 250 WORDS)

L11 ANSWER 6 OF 73 MEDLINE DUPLICATE 5
AN 96038836 MEDLINE
DN 96038836 PubMed ID: 7479024
TI The high stability of the **triple helices** formed between short purine oligonucleotides and SIV/HIV-2 vpx genes is determined by the targeted DNA structure.
AU Svinarchuk F; Monnot M; Merle A; Malvy C; Fermandjian S
CS Laboratoire de Biochimie-Enzymologie, CNRS URA 147, Institut Gustave Roussy, Villejuif, France.
SO NUCLEIC ACIDS RESEARCH, **(1995 Oct 11)** 23 (19) 3831-6.
Journal code: O8L; 0411011. ISSN: 0305-1048.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199511
ED Entered STN: 19960124
Last Updated on STN: 19970203
Entered Medline: 19951130
AB In our previous works we have shown that the oligonucleotides 5'-GGGGAGGGGGAGG-3' and 5'-GGAGGGGGAGGGG-3' give very stable and specific triplexes with their target double stranded DNAs [Svinarchuk, F., Bertrand, J.-R. and Malvy, C. (1994) Nucleic Acids Res., 22, 3742-3747; Svinarchuk, F., Paoletti, J. and Malvy, C. (1995) J. Biol. Chem., 270, 14 068-14,071]. The target for the invariable part of these oligonucleotides, 5'-GGAGGGGGAGG-3', is found in a highly conserved 20 bp long purine/pyrimidine tract of the vpx gene of the SIV and HIV-2 viruses and could be a target for oligonucleotide directed antivirus therapy. Here were report on the ability of four purine oligonucleotides with different lengths (11-, 14-, 17- and 20-mer) to form triplexes with the purine/pyrimidine stretch of the vpx gene. Triplex formation was tested by joint dimethyl **sulfate** (DMS) footprint, gel-retardation assay, circular dichroism (CD) and UV-melting studies. Dimethyl **sulfate** footprint studies revealed the antiparallel orientation of the third strand to the purine strand of the Watson-Crick duplex. However, the protection of the guanines at the ends of the target sequence decreased as the length of the third strand oligonucleotide increased. Melting temperature studies provided profiles with only one transition for all of the triplexes. The melting temperatures of the triplexes were found to be the same as for the targeted duplex in the case of the 11- and 14-mer third strands while for the 17- and 20-mer third strands the melting temperature of the triplexes were correspondingly 4 and 8 degrees C higher than for the duplex. Heating and cooling melting curves were reversible for all of the tested triplexes except one with the 20-mer third strand oligonucleotide. Circular dichroism spectra showed the ability of the target DNA to adopt an A-like DNA conformation. Upon triplex formation the A-DNA form becomes even more pronounced. This effect depends on the length of the third strand oligonucleotide: the CD spectrum shows a 'classical'

A-DNA shape with the 20-mer. This is not observed with the purine/pyrimidine stretch of the HIV-1 DNA which keeps a B-like spectrum even after triplex formation. We suggest, that an A-like duplex DNA is required for the formation of a stable DNA purine(purine-pyrimidine) triplex.

L11 ANSWER 7 OF 73 MEDLINE DUPLICATE 6
AN 95319936 MEDLINE
DN 95319936 PubMed ID: 7596821
TI Overcoming potassium-mediated triplex inhibition.
AU Olivas W M; Maher L J 3rd
CS Eppley Institute for Research in Cancer and Allied Diseases, University of Nebraska Medical Center, Omaha 68198-6805, USA.
NC 5 P30 CA36727-08 (NCI)
GM 47814 (NIGMS)
SO NUCLEIC ACIDS RESEARCH, **(1995 Jun 11)** 23 (11) 1936-41.
Journal code: O8L; 0411011. ISSN: 0305-1048.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199508
ED Entered STN: 19950817
Last Updated on STN: 19950817
Entered Medline: 19950803
AB Sequence-specific duplex DNA recognition by oligonucleotide-directed **triple helix** formation is a possible approach to in vivo gene inhibition. However, **triple helix** formation involving guanine-rich oligonucleotides is inhibited by physiological ions, particularly K+, most likely due to oligonucleotide aggregation via guanine quartets. Three oligodeoxynucleotide (ODN) derivatives were tested for their ability to resist guanine quartet-mediated aggregation, yet form stable triplexes. Electrophoretic mobility shift and dimethyl **sulfate** footprinting assays were used to analyze the formation of triplexes involving these oligonucleotide derivatives. In the absence of K+, all ODNs had similar binding affinities for the duplex target. Triplexes involving a 14mer ODN derivative containing 7-deazaxanthine substituted for three thymine bases or an 18mer ODN containing two additional thymines on both the 5' and 3' termini were abolished by 50 mM K+. Remarkably, triplexes involving an ODN derivative containing four 6-thioguanine bases substituted for guanine resisted K+ inhibition up to 200 mM. We hypothesize that the increased radius and decreased electronegativity of sulfur in the 6-position of guanine destabilize potential guanine quartets. These results improve the prospects for creating ODNS that might serve as specific and efficient gene repressors in vivo.

L11 ANSWER 8 OF 73 MEDLINE
AN 96423126 MEDLINE
DN 96423126 PubMed ID: 8825727
TI Effect of selective cytosine methylation and hydration on the conformations of DNA **triple helices** containing a TTTT loop structure by FT-IR spectroscopy.
AU Fang Y; Bai C; Wei Y; Lin S B; Kan L
CS Institute of Chemistry, Academia Sinica, Beijing, China.
SO JOURNAL OF BIOMOLECULAR STRUCTURE AND DYNAMICS, **(1995 Dec)** 13 (3) 471-82.

Journal code: AH2; 8404176. ISSN: 0739-1102.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199612
ED Entered STN: 19970128
Last Updated on STN: 19970128
Entered Medline: 19961203
AB 5-Methylcytosines have been introduced into triplex-forming-oligonucleotides and shown to extend the pH range over which a triplex forms with a homopurine-homopyrimidine tract of duplex DNA. As a host strand, an oligodeoxypyrimidine with a base sequence of 5'-d(TC)3T4(CT)3 ([CC]) was designed to form a hairpin triplex with a 5'-d-A(GA)2G ([AG6]) purine strand at acidic pH (Tsay, et al., (1995) J. Biomol. Str. Dyn., 13, 1235-1245). We here present results obtained by FT-IR spectroscopy concerning the conformation of the hairpin triplex as a function of the selective substitution of cytosines by 5-methylcytosines in the host strand. Namely, cytosines are substituted by 5-methylcytosines in either the 3'-pyrimidine portion ([CM]) or the 5'-pyrimidine portion ([MC]) or in both ([MM]) of the host strand. The acidic-induced transitions of the equimolar mixtures of the purine target with either of the four pyrimidine oligomers gives rise to different apparent pK values, i.e., [MM].[AG6] (6.2) > [MC].[AG6] (6.0) > [CM].[AG6] (5.7) > [CC].[AG6] (5.2) > single-stranded oligopyrimidines (4.6 +/- 0.2), indicating that cytosine methylation expands the pH range compatible with the hairpin triplex formation regardless of whether the substitution is in the 5'-pyrimidine (Hoogsteen) portion or in the 3'-pyrimidine (Watson-Crick) portion. Thermal denaturation profiles indicated that all the triplexes denatured in a monophasic manner in the pH range of 4.0 to 7.0, and that cytosine methylations in any position of the 16-base pyrimidine oligomer increase the stability of the hairpin triplex DNA. IR spectra recorded in D2O and H2O solutions revealed that cytosine methylation does not significantly influence the conformation of triplex DNA in solution, i.e., all the four triplexes accept a similar sugar conformation, and predominately take on a S-type sugar pucker with a relative proportion of two S-type sugars for one N-type. Furthermore, we also investigated the effect of relative humidity (RH) on the conformation of triplex MC.AG6 in hydrated films, and found that the conformational change induced by the decrease of RH, from predominant S-type to primary N-type sugar pucker, might first occur in the purine strand at 86% RH.

L11 ANSWER 9 OF 73 MEDLINE DUPLICATE 7
AN 95284279 MEDLINE
DN 95284279 PubMed ID: 7766818
TI Solvent effects on model d(CG.G)7 and d(TA.T)7 DNA **triple helices**.
AU Cheng Y K; Pettitt B M
CS Department of Chemistry, University of Houston, TX 77204-5641, USA.
SO BIOPOLYMERS, **(1995 May)** 35 (5) 457-73.
Journal code: A5Z; 0372525. ISSN: 0006-3525.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals

EM 199507
ED Entered STN: 19950713
Last Updated on STN: 19950713
Entered Medline: 19950706
AB Using free energy molecular mechanics, we find that the molecular effects of solvent are critical in determining relative stabilities in DNA **triple helices** or triplexes. The continuum solvent model is unable to differentiate the thermodynamics reflecting the basic solvation differences around the occupied major groove in triplexes. In order to avoid the local minimum problem, which is a major limitation of any modeling study, we started our computations with multiple structures rather than relying on the optimization of a single reference structure. By constructing triplex models with different initial helical twists, helical rises, and sugar-pucker permutations, we explore the potential surface and the structural preference with respect to these variations. We find that in order to accommodate a third strand in triplex formation, the backbone geometry of the B-DNA duplex target has to be adjusted into A-DNA-like form with a deep major groove. This is achieved by concerted adjustment in torsions beta, epsilon, and zeta around the **phosphate** groups. However, the sugar pucker displays a more rich variation, resulting in conformations not usually associated with the canonical duplex structures.

L11 ANSWER 10 OF 73 MEDLINE DUPLICATE 8
AN 95101625 MEDLINE
DN 95101625 PubMed ID: 7803395
TI Fluorescence energy transfer between two **triple helix** -forming oligonucleotides bound to duplex DNA.
AU Mergny J L; Garestier T; Rougee M; Lebedev A V; Chassignol M; Thuong N T; Helene C
CS Laboratoire de Biophysique, Museum National d'Histoire Naturelle, INSERM U201, CNRS UA481, Paris, France.
SO BIOCHEMISTRY, **(1994 Dec 27)** 33 (51) 15321-8.
Journal code: A0G; 0370623. ISSN: 0006-2960.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199501
ED Entered STN: 19950215
Last Updated on STN: 19950215
Entered Medline: 19950127
AB An 11-mer oligopyrimidine was covalently linked via its 5'-**phosphate** to an acridine derivative (acridine-11-mer), and a 13-mer was covalently linked via its 3'-**phosphate** to an ethidium derivative (13-mer-ethidium). Each of them formed a **triple helix** with a 31-bp DNA fragment containing two oligopurine-oligopyrimidine sequences, 11 and 13 bp in length, separated by a variable number of base pairs. When both oligonucleotides were bound to the 31-bp DNA fragment, fluorescence energy transfer (FET) from acridine to ethidium was observed, as revealed by a quenching of acridine fluorescence and a sensitized ethidium emission. FET was temperature-dependent and occurred only when both oligonucleotides were simultaneously bound to the DNA matrix. A single base-pair change in one of the target sequences strongly reduced the energy-transfer efficiency. This method was used to discriminate between a fully complementary and a mismatched target sequence.

=> d his

(FILE 'HOME' ENTERED AT 17:48:25 ON 09 AUG 2001)

FILE 'MEDLINE, BIOSIS' ENTERED AT 17:48:46 ON 09 AUG 2001
L1 0 S TRIPLEX AND (METHYLAMMONIUM OR DIMETHYLAMMONIUM OR TRIMETHYLA
L2 9 S TRIPLEX AND (DIMETHYL SULFOXIDE OR DMSO OR POLYETHYLENE GLYCO
L3 7 DUPLICATE REMOVE L2 (2 DUPLICATES REMOVED)
L4 209 S TRIPLEX AND (PHOSPHATE OR SULFATE OR CYANATE OR ISOCYANATE OR
L5 146 S L4 AND PY<1997
L6 96 DUPLICATE REMOVE L5 (50 DUPLICATES REMOVED)
L7 3 S TRIPLE HELIX AND (METHYLAMMONIUM OR DIMETHYLAMMONIUM OR TRIME
L8 190 S TRIPLE HELIX AND (PHOSPHATE OR SULFATE OR CYANATE OR ISOCYANA
L9 143 S L8 AND PY<1997
L10 119 S L8 AND PY<1996
L11 73 DUPLICATE REMOVE L10 (46 DUPLICATES REMOVED)

=> s l4 and py<1996

L12 113 L4 AND PY<1996

=> duplicate remove l12

DUPLICATE PREFERENCE IS 'MEDLINE, BIOSIS'
KEEP DUPLICATES FROM MORE THAN ONE FILE? Y/(N):n

PROCESSING COMPLETED FOR L12
L13 74 DUPLICATE REMOVE L12 (39 DUPLICATES REMOVED)

=> d bib ab 1-10

L13 ANSWER 1 OF 74 MEDLINE DUPLICATE 1
AN 96066662 MEDLINE
DN 96066662 PubMed ID: 7578100
TI Stabilization of triple-helical nucleic acids by basic oligopeptides.
AU Potaman V N; Sinden R R
CS Institute of Biosciences and Technology, Texas A&M University, Houston 77030-3303, USA.
SO BIOCHEMISTRY, **(1995 Nov 14)** 34 (45) 14885-92.
Journal code: A0G; 0370623. ISSN: 0006-2960.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199512
ED Entered STN: 19960124
Last Updated on STN: 19970203
Entered Medline: 19951218
AB Intermolecular **triplex** DNA is stabilized by metal cations and polyamines which reduce repulsion between the negatively charged **phosphates** of the three nucleic acid strands. We use a quantitative chemical-probing assay involving protection of duplex

guanines in a homopyrimidine.homopurine (Py.Pu) sequence from dimethyl **sulfate** modification to study effects of basic oligopeptides on the stability of **triplex** DNA. An intermolecular protonated pyrimidine.purine.pyrimidine (Py.Pu*Py) **triplex** formed readily between a duplex DNA region and a 14-mer pyrimidine **triplex** -forming oligonucleotide (TFO) at pH 5. The **triplex** was stabilized at pH by the addition of magnesium ions. In the presence of spermine and lysine-rich peptides, the intermolecular **triplex** was stabilized up to pH 6.5-7.0. The effective peptide concentration required for stabilization was 10(-5)-10(-2) M. Of the basic peptides studied, pentalysine (Lys-Lys-Lys-Lys-Lys) was the most effective **triplex** stabilizer. It was effective at concentrations which are lower than those required for Lys-Gly-Lys-Gly-Lys and Lys-Ala-Lys-Ala-Lys and are similar to active concentrations of spermine. Basic peptides were more effective at stabilizing a Py.Pu*Py **triplex** than a pyrimidine.purine.purine (Py.Pu*Pu) **triplex**. At 1 mM, Lys-Lys-Lys-Lys-Lys stabilized the Py.Pu*Pu **triplex** at a level comparable to stabilization by Mn2+ and spermine, whereas Lys-Gly-Lys-Gly-Lys and Lys-Ala-Lys-Ala-Lys resulted in weaker TFO binding. The concentration of TFOs required to form **triplex** DNA were significantly reduced in the presence of peptides.(ABSTRACT TRUNCATED
AT 250 WORDS)

L13 ANSWER 2 OF 74 MEDLINE DUPLICATE 2
AN 95294012 MEDLINE
DN 95294012 PubMed ID: 7775467
TI An unusually stable purine(purine-pyrimidine) short **triplex**. The third strand stabilizes double-stranded DNA.
AU Svinarchuk F; Paoletti J; Malvy C
CS Laboratoire de Biochimie-Enzymologie, CNRS URA 147, Institute Gustave Roussy, Villejuif, France.
SO JOURNAL OF BIOLOGICAL CHEMISTRY, **(1995 Jun 9)** 270 (23) 14068-71.
Journal code: HIV; 2985121R. ISSN: 0021-9258.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199507
ED Entered STN: 19950720
Last Updated on STN: 19950720
Entered Medline: 19950710
AB Classical models for DNA triple helix formation assume the stabilization of these structures through the formation of Hoogsteen hydrogen bonds. This assumes that G-rich duplex DNA is more stable than **triplex** DNA. We report the results of co-migration assay, dimethyl **sulfate** footprint, and UV spectroscopic melting studies that reveal that at least in some cases of short (13-mer) purine(purine-pyrimidine) **triplex** the stability of double-stranded DNA is increased by the binding of the third strand. Under conditions which are usually considered as physiological (10 mM MgCl2, 150 mM Na+ or K+) and with a rate of heating/cooling of 1 degrees C/min, there is a good reversibility of the melting profiles which is consistent with a high rate of **triplex** formation. Other factors than Hoogsteen hydrogen bonds should therefore be
involved in **triplex** stabilization. We suggest that oligonucleotides with similar properties could be efficient agents for artificial gene regulation.

L13 ANSWER 3 OF 74 MEDLINE DUPLICATE 3

AN 96091203 MEDLINE
DN 96091203 PubMed ID: 7501477
TI Single strand targeted **triplex** formation: targeting purine-pyrimidine mixed sequences using abasic linkers.
AU Kandimalla E R; Manning A N; Venkataraman G; Sasisekharan V; Agrawal S
CS Hybridon, Inc., Worcester, MA 01605, USA.
SO NUCLEIC ACIDS RESEARCH, **(1995 Nov 11)** 23 (21) 4510-7.
Journal code: O8L; 0411011. ISSN: 0305-1048.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199601
ED Entered STN: 19960217
Last Updated on STN: 19980206
Entered Medline: 19960117
AB Foldback **triplex**-forming oligonucleotides (FTFOs) that contain an abasic linker, [2-(4-aminobutyr-1-yl)-1,3-propanediol] (APD linker), in the Hoogsteen domain against pyrimidine bases of a C:G and a T:A base pair were studied for their relative stability and sequence specificity of **triplex** formation. In general, the APD linker has less destabilizing effect against a C:G base pair than a T:A base pair. Incorporation of three APD linker moieties resulted in decreased binding to the target, which was comparable to results observed with three imperfectly matched natural base triplets. The APD linker incorporation did not result in the loss of sequence specificity of FTFOs, unlike in the case of normal **triplex**-forming oligonucleotides (TFOs). The introduction of a positively charged abasic linker, however, resulted in decreased stability of the **triplex**, because of loss of hydrogen bonding and stacking interactions in the major groove. The results of a molecular modeling study show that APD linker can be readily incorporated without any change in the conformation of the natural sugar-**phosphate** backbone conserving overall triple helix geometry. Further, the modeling study suggests a hydrogen bond formation between the amino group of linker and N4 of cytosine mediated by a solvent molecule (water) in the floor of the base triplet in addition to a contribution from the positive charge on the APD linker amino group. Either a direct or water-mediated hydrogen bond between the amino group of the APD linker and the O4 of thymine is unlikely when the linker is placed against a T:A base pair.

L13 ANSWER 4 OF 74 MEDLINE DUPLICATE 4
AN 95210279 MEDLINE
DN 95210279 PubMed ID: 7535100
TI Origins of the large differences in stability of DNA and RNA helices: C-5 methyl and 2'-hydroxyl effects.
AU Wang S; Kool E T
CS Department of Chemistry, University of Rochester, New York 14627 USA.
SO BIOCHEMISTRY, **(1995 Mar 28)** 34 (12) 4125-32.
Journal code: A0G; 0370623. ISSN: 0006-2960.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English

FS Priority Journals
EM 199505
ED Entered STN: 19950510
Last Updated on STN: 19960129
Entered Medline: 19950502
AB Recent studies have shown that there can be large differences in the stability of double and triple helical nucleic acid complexes, depending on whether RNA or DNA strands are involved. These differences have been attributed to structural differences in the sugar-**phosphate** backbone of these two polymers. However, since there are in fact two structural features which distinguish DNA from RNA (the 2'-hydroxyl and C-5 methyl groups), the stability differences may arise from either or both of these factors. We have separated effects of the 2'-hydroxyl and C-5 methyl groups by synthesizing nucleic acid strands which contain all possible combinations with and without these groups. Studies of the stabilities of double and triple helices involving these strands show that in fact the C-5 methyl group of thymine and the 2'-OH group of ribose have equally large effects on stability. The two effects vary with secondary structure and can be reinforcing or even opposing in their influence on stability. Three types of complexes are specifically examined: bimolecular pyrimidine.purine duplexes, termolecular pyrimidine.purine.pyrimidine **triplexes**, and bimolecular **triplexes** formed from circular pyrimidine oligonucleotides with purine target strands. It is found in general that the two types of substitutional effects are independent of one another and that C-5 methyl groups are in all cases stabilizing, while 2'-OH groups can be stabilizing or destabilizing, depending on the type of complex. In addition, studies with partially methylated duplexes lend evidence that the largest contribution to stabilization by the methyl group arises from increased base stacking ability rather than from a favorable hydrophobic methyl-methyl contact.(ABSTRACT TRUNCATED AT 250 WORDS)

L13 ANSWER 5 OF 74 MEDLINE DUPLICATE 5
AN 96038836 MEDLINE
DN 96038836 PubMed ID: 7479024
TI The high stability of the triple helices formed between short purine oligonucleotides and SIV/HIV-2 vpx genes is determined by the targeted DNA structure.
AU Svinarchuk F; Monnot M; Merle A; Malvy C; Fermandjian S
CS Laboratoire de Biochimie-Enzymologie, CNRS URA 147, Institut Gustave Roussy, Villejuif, France.
SO NUCLEIC ACIDS RESEARCH, **(1995 Oct 11)** 23 (19) 3831-6.
Journal code: O8L; 0411011. ISSN: 0305-1048.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199511
ED Entered STN: 19960124
Last Updated on STN: 19970203
Entered Medline: 19951130
AB In our previous works we have shown that the oligonucleotides 5'-GGGGAGGGGGAGG-3' and 5'-GGAGGGGGAGGGG-3' give very stable and specific **triplexes** with their target double stranded DNAs [Svinarchuk, F., Bertrand, J.-R. and Malvy, C. (1994) Nucleic Acids Res., 22, 3742-3747; Svinarchuk, F., Paoletti, J. and Malvy, C. (1995) J. Biol. Chem., 270, 14

068-14,071]. The target for the invariable part of these oligonucleotides, 5'-GGAGGGGGAGG-3', is found in a highly conserved 20 bp long purine/pyrimidine tract of the vpx gene of the SIV and HIV-2 viruses and could be a target for oligonucleotide directed antivirus therapy. Here were report on the ability of four purine oligonucleotides with different lengths (11-, 14-, 17- and 20-mer) to form **triplexes** with the purine/pyrimidine stretch of the vpx gene. **Triplex** formation was tested by joint dimethyl **sulfate** (DMS) footprint, gel-retardation assay, circular dichroism (CD) and UV-melting studies. Dimethyl **sulfate** footprint studies revealed the antiparallel orientation of the third strand to the purine strand of the Watson-Crick duplex. However, the protection of the guanines at the ends of the target sequence decreased as the length of the third strand oligonucleotide increased. Melting temperature studies provided profiles with only one transition for all of the **triplexes**. The melting temperatures of the **triplexes** were found to be the same as for the targeted duplex in the case of the 11- and 14-mer third strands while for the 17- and 20-mer third strands the melting temperature of the **triplexes** were correspondingly 4 and 8 degrees C higher than for the duplex. Heating and cooling melting curves were reversible for all of the tested **triplexes** except one with the 20-mer third strand oligonucleotide. Circular dichroism spectra showed the ability of the target DNA to adopt an A-like DNA conformation. Upon **triplex** formation the A-DNA form becomes even more pronounced. This effect depends on the length of the third strand oligonucleotide: the CD spectrum shows a 'classical' A-DNA shape with the 20-mer. This is not observed with the purine/pyrimidine stretch of the HIV-1 DNA which keeps a B-like spectrum even after **triplex** formation. We suggest, that an A-like duplex DNA is required for the formation of a stable DNA purine(purine-pyrimidine) **triplex**.

L13 ANSWER 6 OF 74 MEDLINE DUPLICATE 6
AN 95319936 MEDLINE
DN 95319936 PubMed ID: 7596821
TI Overcoming potassium-mediated **triplex** inhibition.
AU Olivas W M; Maher L J 3rd
CS Eppley Institute for Research in Cancer and Allied Diseases, University of Nebraska Medical Center, Omaha 68198-6805, USA.
NC 5 P30 CA36727-08 (NCI)
GM 47814 (NIGMS)
SO NUCLEIC ACIDS RESEARCH, **(1995 Jun 11)** 23 (11) 1936-41.
Journal code: O8L; 0411011. ISSN: 0305-1048.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199508
ED Entered STN: 19950817
Last Updated on STN: 19950817
Entered Medline: 19950803
AB Sequence-specific duplex DNA recognition by oligonucleotide-directed triple helix formation is a possible approach to in vivo gene inhibition. However, triple helix formation involving guanine-rich oligonucleotides is inhibited by physiological ions, particularly K+, most likely due to oligonucleotide aggregation via guanine quartets. Three oligodeoxynucleotide (ODN) derivatives were tested for their ability to

resist guanine quartet-mediated aggregation, yet form stable **triplexes**. Electrophoretic mobility shift and dimethyl **sulfate** footprinting assays were used to analyze the formation of **triplexes** involving these oligonucleotide derivatives. In the absence of K+, all ODNs had similar binding affinities for the duplex target. **Triplexes** involving a 14mer ODN derivative containing 7-deazaxanthine substituted for three thymine bases or an 18mer ODN containing two additional thymines on both the 5' and 3' termini were abolished by 50 mM K+. Remarkably, **triplexes** involving an ODN derivative containing four 6-thioguanine bases substituted for guanine resisted K+ inhibition up to 200 mM. We hypothesize that the increased radius and decreased electronegativity of sulfur in the 6-position of guanine destabilize potential guanine quartets. These results improve the prospects for creating ODNS that might serve as specific and efficient gene repressors in vivo.

L13 ANSWER 7 OF 74 BIOSIS COPYRIGHT 2001 BIOSIS
AN 1995:484193 BIOSIS
DN PREV199598498493
TI Dielectric response of **triplex** DNA in ionic solution from simulations.
AU Yang, Liqui; Weerasinghe, Samantha; Smith, Paul E.; Pettitt, B. Montgomery
(1)
CS (1) Dep. Chem., Univ. Houston, Houston, TX 77204-5641 USA
SO Biophysical Journal, (1995) Vol. 69, No. 4, pp. 1519-1527. ISSN: 0006-3495.
DT Article
LA English
AB We have analyzed a 1.2-ns molecular dynamics simulation of 51 mM d(CG cntdot G)-7 with 21 Na+ counter-ions and 1 M NaCl in water. Via the dipole fluctuations, the dielectric constant for the DNA is found to be around 16, whereas that for the bases and sugars combined is only 3. The dielectric constant for water in this system is 41, which is much smaller than 71 for pure SPC/E water, because of the strong restriction imposed on the motion of water molecules by the DNA and the ions. Also addressed in the present work are several technical issues related to the calculation of the dipole moment of an ionic solution from molecular dynamics simulations using periodic boundary conditions.

L13 ANSWER 8 OF 74 MEDLINE DUPLICATE 7
AN 95239759 MEDLINE
DN 95239759 PubMed ID: 7723038
TI Probing the structure of a putative intermediate in homologous recombination: the third strand in the parallel DNA **triplex** is in contact with the major groove of the duplex.
AU Kim M G; Zhurkin V B; Jernigan R L; Camerini-Otero R D
CS Genetics and Biochemistry Branch, National Institute of Diabetes and Digestive and Kidney Diseases, National Institutes of Health, Bethesda, MD 20892-1810, USA.
SO JOURNAL OF MOLECULAR BIOLOGY, **(1995 Apr 14)** 247 (5) 874-89. Journal code: J6V; 2985088R. ISSN: 0022-2836.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199505

ED Entered STN: 19950605
Last Updated on STN: 19950605
Entered Medline: 19950525

AB A three-stranded DNA that is a putative intermediate of homologous recombination is a novel DNA **triplex**, R-form DNA. In R-form DNA the third strand includes both purines and pyrimidines and is parallel to the identical strand of the duplex. To test and refine our previously proposed R-form base triplets we have used two approaches: (1) dimethyl **sulfate** protection of R-form DNA; and (2) thermal dissociation of R-form DNAs in which the duplex strands were substituted in a strand-specific manner with either 7-deaza-guanine or 7-deaza-adenine. Together, the footprinting and isosteric substitution results demonstrate that the third strand in R-form DNA is in contact with the purines in the N7 position in the major groove of the Watson-Crick duplex in three ((GC):G, (AT):A and (TA):T) out of the four possible triplets. Furthermore, these results suggest that the N7 positions of the duplex play a significant role in stabilizing the DNA-DNA contacts during the homology recognition process.

L13 ANSWER 9 OF 74 MEDLINE
AN 96423126 MEDLINE
DN 96423126 PubMed ID: 8825727
TI Effect of selective cytosine methylation and hydration on the conformations of DNA triple helices containing a TTTT loop structure by FT-IR spectroscopy.
AU Fang Y; Bai C; Wei Y; Lin S B; Kan L
CS Institute of Chemistry, Academia Sinica, Beijing, China.
SO JOURNAL OF BIOMOLECULAR STRUCTURE AND DYNAMICS, **(1995 Dec)** 13 (3) 471-82.
Journal code: AH2; 8404176. ISSN: 0739-1102.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199612
ED Entered STN: 19970128
Last Updated on STN: 19970128
Entered Medline: 19961203

AB 5-Methylcytosines have been introduced into **triplex** -forming-oligonucleotides and shown to extend the pH range over which a **triplex** forms with a homopurine-homopyrimidine tract of duplex DNA. As a host strand, an oligodeoxypyrimidine with a base sequence of 5'-d(TC)3T4(CT)3 ([CC]) was designed to form a hairpin **triplex** with a 5'-d-A(GA)2G ([AG6]) purine strand at acidic pH (Tsay, et al., (1995) J. Biomol. Str. Dyn., 13, 1235-1245). We here present results obtained by FT-IR spectroscopy concerning the conformation of the hairpin **triplex** as a function of the selective substitution of cytosines by 5-methylcytosines in the host strand. Namely, cytosines are substituted by 5-methylcytosines in either the 3'-pyrimidine portion ([CM]) or the 5'-pyrimidine portion ([MC]) or in both ([MM]) of the host strand. The acidic-induced transitions of the equimolar mixtures of the purine target with either of the four pyrimidine oligomers gives rise to different apparent pK values, i.e., [MM].[AG6] (6.2) > [MC].[AG6] (6.0) > [CM].[AG6] (5.7) > [CC].[AG6] (5.2) > single-stranded oligopyrimidines (4.6 +/- 0.2), indicating that cytosine methylation expands the pH range compatible with the hairpin **triplex** formation regardless of whether the substitution is in the 5'-pyrimidine (Hoogsteen) portion or in the

3'-pyrimidine (Watson-Crick) portion. Thermal denaturation profiles indicated that all the **triplexes** denatured in a monophasic manner in the pH range of 4.0 to 7.0, and that cytosine methylations in any position of the 16-base pyrimidine oligomer increase the stability of the hairpin **triplex** DNA. IR spectra recorded in D2O and H2O solutions revealed that cytosine methylation does not significantly influence the conformation of **triplex** DNA in solution, i.e., all the four **triplexes** accept a similar sugar conformation, and predominately take on a S-type sugar pucker with a relative proportion of two S-type sugars for one N-type. Furthermore, we also investigated the effect of relative humidity (RH) on the conformation of **triplex** MC.AG6 in hydrated films, and found that the conformational change induced by the decrease of RH, from predominant S-type to primary N-type sugar pucker, might first occur in the purine strand at 86% RH.

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TI Solvent effects on model d(CG.G)7 and d(TA.T)7 DNA triple helices.
AU Cheng Y K; Pettitt B M
CS Department of Chemistry, University of Houston, TX 77204-5641, USA.
SO BIOPOLYMERS, **(1995 May)** 35 (5) 457-73.
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DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
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AB Using free energy molecular mechanics, we find that the molecular effects of solvent are critical in determining relative stabilities in DNA triple helices or **triplexes**. The continuum solvent model is unable to differentiate the thermodynamics reflecting the basic solvation differences around the occupied major groove in **triplexes**. In order to avoid the local minimum problem, which is a major limitation of any modeling study, we started our computations with multiple structures rather than relying on the optimization of a single reference structure. By constructing **triplex** models with different initial helical twists, helical rises, and sugar-pucker permutations, we explore the potential surface and the structural preference with respect to these variations. We find that in order to accommodate a third strand in **triplex** formation, the backbone geometry of the B-DNA duplex target has to be adjusted into A-DNA-like form with a deep major groove. This is achieved by concerted adjustment in torsions beta, epsilon, and zeta around the **phosphate** groups. However, the sugar pucker displays a more rich variation, resulting in conformations not usually associated with the canonical duplex structures.

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FULL ESTIMATED COST	28.59	28.74

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